```
          1                                                  50
EG327     MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVATAVLA TLLFATVQAS.
BZ198     MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLFATVQAN
BZ10      MNKISRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLFATVQAN
H15       MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLFATVQAN
EG329     MNEILRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
PMC21     MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
H38       MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
P20       MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVATAVLA TLLSATVQAN
Z2491     MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
H41       MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
Consensus MN-I-RIIWN SALNAWV-VS ELTRNHTKRA SATV-TAVLA TLL-ATVQA-
                                                     C1

          51                                                 100
EG327     TTDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.VTED SNWGVYFDKK
BZ198     ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
BZ10      ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
H15       ATDDD...DL YLEPVQRTAV VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
EG329     ANNEEQEEDL YLDPVLRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
PMC21     ANNEEQEEDL YLDPVQRTVA VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
H38       ATDED..EEE ELEPVVRSAL VLQFMIDKEG NGENE.STGN IGWSIYYDNH
P20       ATDTD..EDE ELESVARSAL VLQFMIDKEG NGEIESTGDI GWSIYYDDHN
Z2491     ATDED..EEE ELESVQR.SV VGSIQASMEG SGELET...I SLSMTNDSKE
H41       ATDED..EEE ELESVQR.SV VGSIQASMEG SVELET...I SLSMTNDSKE
Consensus ---------- -L--V-R--- V-------EG --E-E----- ----------
                                                     V1

          101                                                150
EG327     GVLTAGTITL KAGDNLKIKQ NTNENTNASS ....FTYSLK KDLTDLTSVG
BZ198     RVLKAGAITL KAGDNLKIKQ NTNENTNDSS ....FTYSLK KDLTDLTSVE
BZ10      RVLKAGAITL KAGDNLKIKQ NTNENTNENT NDSSFTYSLK KDLTDLTSVE
H15       RVLKAGAITL KAGDNLKIKQ NTNENTNENT NDSSFTYSLK KDLTDLTSVE
EG329     GVLTAREITL KAGDNLKIKQ NG...TN... ....FTYSLK KDLTDLTSVG
PMC21     GVLTAREITL KAGDNLKIKQ NG...TN... ....FTYSLK KDLTDLTSVG
H38       NTLHGATVTL KAGDNLKIKQ NTNKNTNENT NDSSFTYSLK KDLTDLTSVE
P20       TLHG.ATVTL KAGDNLKIKQ SGKD..... ....FTYSLK KELKDLTSVE
Z2491     FVDPYIVVTL KAGDNLKIKQ NTNENTNASS ....FTYSLK KDLTGLINVE
H41       FVDPYIVVTL KAGDNLKIKQ NTNENTNASS ....FTYSLK KDLTGLINVE
Consensus ---------TL KAGDNLKIKQ ---------- ----FTYSLK K-L--L--V-
          V1          C2          V2                C3

          151                                                200
EG327     TEKLSFSANS NKVNITSDTK GLNFAKKTAE TNGDTTVHLN GIGSTLTDTL
BZ198     TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
BZ10      TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H15       TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
EG329     TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL
PMC21     TEKLSFSANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL
H38       TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL
P20       TEKLSFGANG NKVNITSDTK GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
Z2491     TEKLSFGANG KKVNIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL
H41       TEKLSFGANG KKVNIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML
Consensus TEKLSF-AN- -KVNI-SDTK GLNFAK-TA- TNGD-TVHLN GIGSTLTD-L
                                                     C3
```

FIG. 1

	201				250
EG327	LNTGATTNVT	NDNVTDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
BZ198	LNTGATTNVT	NDNVTDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
BZ10	LNTGATTNVT	NDNVTDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
H15	LNTGATTNVT	NDNVTDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
EG329	LNTGATTNVT	NDNVTDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
PMC21	LNTGATTNVT	NDNVTDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
H38	LNTGATTNVT	NDNVTDDKKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
P20	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVKT	GSTTGQSENV
Z2491	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVKT	GSTTGQSENV
H41	LNTGATTNVT	NDNVTDDEKK	RAASVKDVLN	AGWNIKGVKP	GTTAS..DNV
Consensus	----A-----	----T-----	RAAS-KDVLN	AGWNIKGVK-	G-T-----NV
	V3		C4		V4

	251				300
EG327	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGKL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
H15	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGKL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGKL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGKL
H38	DFVHTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
P20	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
H41	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGKL
Consensus	DFV-TYDTVE	FLSADTKTTT	VNVESKDNGK	-TEVKIGAKT	SVIKEKDGKL
			C5		

	301				350
EG327	VTGKDKGEND	SSTDKGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
BZ198	VTGKGKDENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
BZ10	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
H15	VTGKGKDENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
EG329	VTGKDKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
PMC21	VTGKDKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
H38	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
P20	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
Z2491	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
H41	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
Consensus	VTGK-K-EN-	SSTD-GEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
			C5		

	351				400
EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVMYDVNVGD	ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
BZ10	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
H15	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVMYDVNVGD	ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVMYDVNVGD	ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
P20	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI	TVMYDVNVGD	ALNVNQLQNS
H41	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI	TVKYDVNVGD	ALNVNQLQNS
Consensus	FETVTSGT-V	TFASG-GTTA	TVSKDDQGNI	TV-YDVNVGD	ALNVNQLQNS
			C5		

FIG. 1 cont.

```
                401                                                   450
EG327   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ198   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID
 BZ10   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID
  H15   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID
EG329   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID
PMC21   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID
  H38   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID
  P20   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID
Z2491   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EISRNGKNID
  H41   GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EITRNGKNID
Consensus GWNLDSKAVA GSSGKVISGN VSPSKGKMDE TVNINAGNNI EI-RNGKNID
                                                      C5

                451                                                   500
EG327   IATSMTPQFS SVSLGAGADA PTLSVDDEGA LNVGSKDANK PVRITNVAPG
BZ198   IATSMAPQFS SVSLGAGADA PTLSVDDEGA LNVGSKDTNK PVRITNVAPG
 BZ10   IATSMTPQFS SVSLGAGADA PTLSVDDEGA LNVGSKDANK PVRITNVAPG
  H15   IATSMTPQFS SVSLGAGADA PTLSVDDEGA LNVGSKDANK PVRITNVAPG
EG329   IATSMTPQFS SVSLGAGADA PTLSVDG.DA LNVGSKKDNK PVRITNVAPG
PMC21   IATSMTPQFS SVSLGAGADA PTLSVDG.DA LNVGSKKDNK PVRITNVAPG
  H38   IATSMTPQFS SVSLGAGADA PTLSVDDKGA LNVGSKDANK PVRITNVAPG
  P20   IATSMTPQFS SVSLGAGADA PTLSVDDEGA LNVGSKDANK PVRITNVAPG
Z2491   IATSMAPQFS SVSLGAGADA PTLSVDDEGA LNVGSKDANK PVRITNVAPG
  H41   IATSMTPQFS SVSLGAGADA PTLSVDDEGA LNVGSKDANK PVRITNVAPG
Consensus IATSM-PQFS SVSLGAGADA PTLSVD---A LNVGSK--NK PVRITNVAPG
                                                      C5

                501                                                   550
EG327   VKEGDVTNVA QLKGVAQNLN NHIDNVDGNA RAGIAQAIAT AGLVQAYLPG
BZ198   VKEGDVTNVA QLKGVAQNLN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
 BZ10   VKEGDVTNVA QLKGVAQNLN NRIDNVDGNA RAGIAQAIAT AGLAQAYLPG
  H15   VKEGDVTNVA QLKGVAQNLN NRIDNVDGNA RAGIAQAIAT AGLAQAYLPG
EG329   VKEGDVTNVA QLKGVAQNLN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
PMC21   VKEGDVTNVA QLKGVAQNLN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
  H38   VKEGDVTNVA QLKGVAQNLN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
  P20   VKEGDVTNVA QLKGVAQNLN NRIDNVNGNA RAGIAQAIAT AGLAQAYLPG
Z2491   VKEGDVTNVA QLKGVAQNLN NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
  H41   VKEGDVTNVA QLKGVAQNLN NRIDNVNGNA RAGIAQAIAT AGLVQAYLPG
Consensus VKEGDVTNVA QLKGVAQNLN N-IDNV-GNA RAGIAQAIAT AGL-QAYLPG
                                                      C5

                551                                                   600
EG327   KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
BZ198   KSMMAIGGDT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
 BZ10   KSMMAIGGGT YRGEAGYAIG YSSISDTGNW VIKGTASGNS RGHFGTSASV
  H15   KSMMAIGGGT YRGEAGYAIG YSSISDTGNW VIKGTASGNS RGHFGASASV
EG329   KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
PMC21   KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
  H38   KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
  P20   KSMMAIGGGT YLGEAGYAIG YSSISDTGNW VIKGTASGNS RGHFGTSASV
Z2491   KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS RGHFGASASV
  H41   KSMMAIGGGT YLGEAGYAIG YSSISAGGNW IIKGTASGNS RGHFGASASV
Consensus KSMMAIGG-T Y-GEAGYAIG YSSIS--GNW -IKGTASGNS RGHFG-SASV
                                                      C5
```

FIG. 1 cont.

	601
EG327	GYQW.
BZ198	GYQW.
BZ10	GYQW.
H15	GYQW.
EG329	GYQW.
PMC21	GYQW.
H38	GYQW.
P20	GYQW.
Z2491	GYQW.
H41	GYQW.
Consensus	GYQW.
	C5

FIG. 1 cont.

```
          1                                                                  70
H15       ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
BZ10      ATGAACAAAA TATCCCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
BZ198     ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
P20       ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT AGTCGTATCC GAGCTCACAC
H38       ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
Z2491     ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
H41       ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
EG329     ATGAACGAAA TATTGCGCAT CATTTGGAAT AGCGCCCTCA ATGCCTGGGT CGTTGTATCC GAGCTCACAC
PMC21     ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT CGTCGTATCC GAGCTCACAC
EG327     ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
Consensus ATGAAC-AAA TAT--CGCAT CATTTGGAAT AG-GCCCTCA ATGC-TGGGT -G--GTATCC GAGCTCACAC
                                          C1

          71                                                                 140
H15       GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
BZ10      GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
BZ198     GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
P20       GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGCTGT CCGCAACGGT
H38       GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACGCTGTTGT TTGCAACGGT
Z2491     GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
H41       GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
EG329     GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
PMC21     GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
EG327     GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT
Consensus GCAACCACAC CAAACGCGCC TCCGCAACCG TG--GACCGC CGTATTGGCG AC-CTG-TGT --GCAACGGT
                                          C1

          141                                                                210
H15       TCAGGCGAAT GCTACCGATG ACGAC..... ....GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
BZ10      TCAGGCGAAT GCTACCGATG ACGAC..... ....GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
BZ198     TCAGGCGAAT GCTACCGATG ACGAC..... ....GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
P20       TCAGGCGAAT GCTACCGATA CCGAT..... .GAAGATGAA GAGTTAGAAT CCGTAGCACG CTCTGCTCTG
H38       TCAGGCGAAT GCTACCGATG AAGAT..... .GAAGAAGAA GAGTTAGAAC CCGTAGTACG CTCTGCTCTG
Z2491     TCAGGCGAAT GCTACCGATG AAGAT..... .GAAGAAGAA GAGTTAGAAT CCGTACAACG CTCTGTCGTA
H41       TCAGGCGAAT GCTACCGATG AAGAT..... .GAAGAAGAA GAGTTAGAAT CCGTACAACG CTCTG...TC
EG329     TCAGGCAAGT GCTAACAATG AAGAGCAAGA AGAAGATTTA TATTTAGACC CCGTGCTACG CACTGTTGCC
PMC21     TCAGGCAAGT GCTAACAATG AAGAGCAAGA AGAAGATTTA TATTTAGACC CCGTACAACG CACTGTTGCC
EG327     TCAGGCGAGT ACTACCGATG ACGAC..... ....GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
Consensus TCAGGC-A-T -CTA-C-AT- --GA------ ----GA---A -A-TTAGA-- CCGT---ACG C-CTG-----
            C1                                V1

          211                                                                280
H15       GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
BZ10      GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
BZ198     GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
P20       GTGTTGCAAT TCATGATCGA TAAAGAAGGC AATGGAGAAA TCGAATCTAC AGGAGA...T ATAGGTTGGA
H38       GTGTTGCAAT TCATGATCGA TAAAGAAGGC AATGGAGAAA ACGAATCTAC AGGAAA...T ATAGGTTGGA
Z2491     GGG..AGCAT TCAAG.CCAG TATGGAAGGC AGCGGCGAAT TGGAAACGAT ATCAT....T ATCAATGACT
H41       GTAGGGAGCA TTCAAGCCAG TATGGAAGGC AGCGTCGAAT TGGAAACGAT A......... TCATTATCAA
EG329     GTGTTGATAG TCAATTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAAAAGT AGAAGAAAAT TCAGATTGGG
PMC21     GTGTTGATAG TCAATTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAAAAGT AGAAGAAAAT TCAGATTGGG
EG327     GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGTTAC AGAAGA...T TCAAATTGGG
Consensus G---------- T------C-- TA--GAAGGC A--G--GAA- --GAA----- A---------- ----------
                                            V1
```

FIG. 2

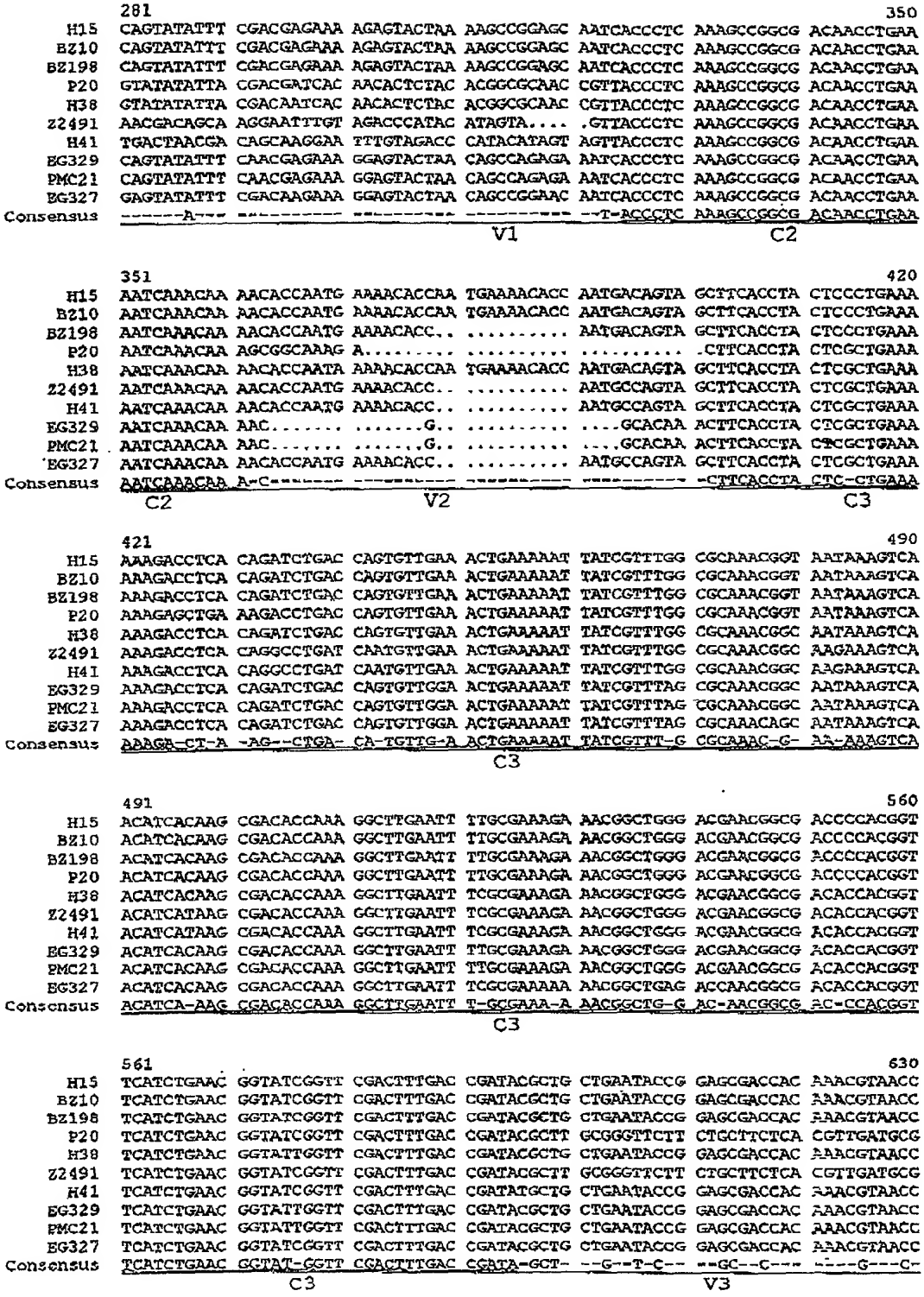
281
350
H15 CAGTATATTT CGACGAGAAA AGAGTACTAA AAGCCGGAGC AATCACCCTC AAAGCCGGCG ACAACCTGAA
BZ10 CAGTATATTT CGACGAGAAA AGAGTACTAA AAGCCGGAGC AATCACCCTC AAAGCCGGCG ACAACCTGAA
BZ198 CAGTATATTT CGACGAGAAA AGAGTACTAA AAGCCGGAGC AATCACCCTC AAAGCCGGCG ACAACCTGAA
P20 GTATATATTA CGACGATCAC AACACTCTAC ACGGCGCAAC CGTTACCCTC AAAGCCGGCG ACAACCTGAA
H38 GTATATATTA CGACAATCAC AACACTCTAC ACGGCGCAAC CGTTACCCTC AAAGCCGGCG ACAACCTGAA
Z2491 AACGACAGCA AGGAATTTGT AGACCCATAC ATAGTA.... .GTTACCCTC AAAGCCGGCG ACAACCTGAA
H41 TGACTAACGA CAGCAAGGAA TTTGTAGACC CATACATAGT AGTTACCCTC AAAGCCGGCG ACAACCTGAA
EG329 CAGTATATTT CAACGAGAAA GGAGTACTAA CAGCCAGAGA AATCACCCTC AAAGCCGGCG ACAACCTGAA
PMC21 CAGTATATTT CAACGAGAAA GGAGTACTAA CAGCCAGAGA AATCACCCTC AAAGCCGGCG ACAACCTGAA
EG327 GAGTATATTT CGACAAGAAA GGAGTACTAA CAGCCGGAAC AATCACCCTC AAAGCCGGCG ACAACCTGAA
Consensus ------A--- ---------- ---------- ---------- --T-ACCCTC AAAGCCGGCG ACAACCTGAA
V1
C2
351
420
H15 AATCAAACAA AACACCAATG AAAACACCAA TGAAAACACC AATGACAGTA GCTTCACCTA CTCCCTGAAA
BZ10 AATCAAACAA AACACCAATG AAAACACCAA TGAAAACACC AATGACAGTA GCTTCACCTA CTCCCTGAAA
BZ198 AATCAAACAA AACACCAATG AAAACACC.. .... AATGACAGTA GCTTCACCTA CTCCCTGAAA
P20 AATCAAACAA AGCGGCAAAG A......... .... .CTTCACCTA CTCGCTGAAA
H38 AATCAAACAA AACACCAATA AAAACACCAA TGAAAACACC AATGACAGTA GCTTCACCTA CTCGCTGAAA
Z2491 AATCAAACAA AACACCAATG AAAACACC.. .... AATGCCAGTA GCTTCACCTA CTCGCTGAAA
H41 AATCAAACAA AACACCAATG AAAACACC.. .... AATGCCAGTA GCTTCACCTA CTCGCTGAAA
EG329 AATCAAACAA AAC..... ....G.. ....GCACAA ACTTCACCTA CTCGCTGAAA
PMC21 AATCAAACAA AAC..... ....G.. ....GCACAA ACTTCACCTA CTCGCTGAAA
EG327 AATCAAACAA AACACCAATG AAAACACC.. .... AATGCCAGTA GCTTCACCTA CTCGCTGAAA
Consensus AATCAAACAA A-C------- ---------- ---------- ---------- -CTTCACCTA CTC-CTGAAA
C2
V2
C3
421
490
H15 AAAGACCTCA CAGATCTGAC CAGTGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
BZ10 AAAGACCTCA CAGATCTGAC CAGTGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
BZ198 AAAGACCTCA CAGATCTGAC CAGTGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
P20 AAAGAGCTGA AAGACCTGAC CAGTGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
H38 AAAGACCTCA CAGATCTGAC CAGTGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGC AATAAAGTCA
Z2491 AAAGACCTCA CAGGCCTGAT CAATGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGC AAGAAAGTCA
H41 AAAGACCTCA CAGGCCTGAT CAATGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGC AAGAAAGTCA
EG329 AAAGACCTCA CAGATCTGAC CAGTGTTGGA ACTGAAAAAT TATCGTTTAG CGCAAACGGC AATAAAGTCA
PMC21 AAAGACCTCA CAGATCTGAC CAGTGTTGGA ACTGAAAAAT TATCGTTTAG CGCAAACGGC AATAAAGTCA
EG327 AAAGACCTCA CAGATCTGAC CAGTGTTGGA ACTGAAAAAT TATCGTTTAG CGCAAACAGC AATAAAGTCA
Consensus AAAGA-CT-A -AG--CTGA- CA-TGTTG-A ACTGAAAAAT TATCGTTT-G CGCAAAC-G- AA-AAAGTCA
C3
491
560
H15 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
BZ10 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
BZ198 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
P20 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
H38 ACATCACAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
Z2491 ACATCATAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
H41 ACATCATAAG CGACACCAAA GGCTTGAATT TCGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
EG329 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
PMC21 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
EG327 ACATCACAAG CGACACCAAA GGCTTGAATT TCGCGAAAAA AACGGCTGAG ACCAACGGCG ACACCACGGT
Consensus ACATCA-AAG CGACACCAAA GGCTTGAATT T-GCGAAA-A AACGGCTG-G AC-AACGGCG AC-CCACGGT
C3
561
630
H15 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
BZ10 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
BZ198 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
P20 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG
H38 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
Z2491 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG
H41 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATATGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
EG329 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
PMC21 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
EG327 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
Consensus TCATCTGAAC GCTAT-GGTT CGACTTTGAC CGATA-GCT- --G--T-C-- --GC--C--- ----G---C-
C3
V3

FIG. 2 cont.

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                631                                                                 700
H15     AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
BZ10    AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
BZ198   AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
P20     GGTAACCAAA GTACACATTA C......ACT CGTGCAGCAA GTATTAAGGA TGTGTTGAAT GCGGGTTGGA
H38     AACGACAACG TTACCGATGA CAAGAAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
Z2491   GGTAACCAAA GTACACATTA C......ACT CGTGCAGCAA GTATTAAGGA TGTGTTGAAT GCGGGTTGGA
H41     AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
EG329   AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCTGGCTGGA
PMC21   AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCTGGCTGGA
EG327   AACGACAACG TTACCGATGA CGAGAAAAAA CGTGCGGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
Consensus ----AC-A-- -TAC--AT-A C------A-- CGTGC-GCAA G--TTAA-GA -GT-TT-AA- GC-GG-TGGA
                     V3                                                  C4

                701                                                                 770
H15     ACATTAAAGG CGTTAAACCC GGTACAACAG CT......TC CGATAACGTT GATTTCGTCC GCACTTACGA
BZ10    ACATTAAAGG CGTTAAACCC GGTACAACAG CT......TC CGATAACGTC GATTTCGTCC GCACTTACGA
BZ198   ACATTAAAGG CGTTAAACCC GGTACAACAG CT......TC CGATAACGTT GATTTCGTCC GCACTTACGA
P20     ATATTAAGGG TGTTAAAACT GGCTCAACAA CTGGTCAATC AGAAAATGTC GATTTCGTCC GCACTTACGA
H38     ACATTAAAGG CGTTAAACCC GGTACAACAG CT......TC CGATAACGTT GATTTCGTCC ACACTTACGA
Z2491   ATATTAAGGG TGTTAAAACT GGCTCAACAA CTGGTCAATC AGAAAATGTC GATTTCGTCC GCACTTACGA
H41     ACATTAAAGG CGTTAAACCC GGTACAACAG CT......TC CGATAACGTT GATTTCGTCC GCACTTACGA
EG329   ACATTAAAGG CGTTAAACCC GGTACAACAG CT......TC CGATAACGTT GATTTCGTCC GCACTTACGA
PMC21   ACATTAAAGG CGTTAAACCC GGTACAACAG CT......TC CGATAACGTT GATTTCGTCC GCACTTACGA
EG327   ACATTAAAGG CGTTAAACCC GGTACAACAG CT......TC CGATAACGTT GATTTCGTCC GCACTTACGA
Consensus A-ATTAA-GG -GTTAAA-C- GG--CAACA- CT-------TC -GA-AA-GT- GATTTCGTCC -GACTTACGA
          C4          V4                                              C5

                771                                                                 840
H15     CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
BZ10    CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
BZ198   CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
P20     CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
H38     CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
Z2491   CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
H41     CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
EG329   CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
PMC21   CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
EG327   CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
Consensus CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
                                    C5

                841                                                                 910
H15     AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
BZ10    AGAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
BZ198   AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
P20     AGAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
H38     AGAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
Z2491   AGAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
H41     AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
EG329   AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
PMC21   AAAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
EG327   AGAACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTATCA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
Consensus A-AACCGAAG TTAAAATCGG TGCGAAGACT TCTGTTAT-A AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
                                    C5

                911                                                                 980
H15     AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
BZ10    AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
BZ198   AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
P20     AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
H38     AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
Z2491   AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
H41     AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
EG329   AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
PMC21   AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
EG327   AAGACAAAGG CGAGAATGAT TCTTCTACAG ACAAAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
Consensus AAG-CAAAG- CGAGAATG-T TCTTCTACAG AC-AAGGCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
                                    C5
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FIG. 2 cont.

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          981                                                                1050
H15       TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
BZ10      TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
BZ198     TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
P20       TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
H38       TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
Z2491     TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
H41       TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
EG329     TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
PMC21     TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
EG327     TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
Consensus TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
                                                                      C5

          1051                                                               1120
H15       TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACTGCG ACTGTAAGTA
BZ10      TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACTGCG ACTGTAAGTA
BZ198     TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACTGCG ACTGTAAGTA
P20       TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACTGCG ACTGTAAGTA
H38       TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACTGCG ACTGTAAGTA
Z2491     TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACTGCG ACTGTAAGTA
H41       TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACTGCG ACTGTAAGTA
EG329     TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACTGCG ACTGTAAGTA
PMC21     TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACTGCG ACTGTAAGTA
EG327     TTTGAAACCG TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACTGCG ACTGTAAGTA
Consensus TTTGAAACCG TTACATCAGG CACAAA-GTA ACCTTTGCTA GTGGTAA-GG TACAACTGCG ACTGTAAGTA
                                                                      C5

          1121                                                               1190
H15       AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
BZ10      AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
BZ198     AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
P20       AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
H38       AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
Z2491     AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
H41       AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
EG329     AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
PMC21     AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
EG327     AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
Consensus AAGATGATCA AGGCAACATC ACTGTTA-GT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
                                                                      C5

          1191                                                               1260
H15       GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
BZ10      GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
BZ198     GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
P20       GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
H38       GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
Z2491     GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
H41       GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
EG329     GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
PMC21     GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
EG327     GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
Consensus GCAAAACAGC GGTTGGAATT TGGATTCCAA AGCGGTTGCA GGTTCTTCGG GCAAAGTCAT CAGCGGCAAT
                                                                      C5

          1261                                                               1330
H15       GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
BZ10      GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
BZ198     GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
P20       GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
H38       GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Z2491     GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTAGCC
H41       GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG329     GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
PMC21     GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG327     GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Consensus GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTA-CC
                                                                      C5
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FIG. 2 cont.

```
          1331                                                                        1400
      H15 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
     BZ10 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
    BZ198 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGGCGCC GCAGTTTTCC AGCGTTTCGC TCGGTGCGGG
      P20 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
      H38 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAGTTTTCC AGCGTTTCGC TCGGCGCGGG
    Z2491 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGGCGCC GCAGTTTTCC AGCGTTTCGC TCGGCGCGGG
      H41 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
    EG329 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAGTTTTCC AGCGTTTCGC TCGGCGCGGG
    PMC21 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAGTTTTCC AGCGTTTCGC TCGGCGCGGG
    EG327 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
Consensus GCAACGG-AA AAATATCGAC ATCGCCACTT CGATG-C-CC GCA-TTTTCC AGCGTTTCGC TCGG-GCGGG
                                               C5

          1401                                                                        1470
      H15 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
     BZ10 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
    BZ198 GGCGGATGCG CCCACTTTGA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TACCAACAAA
      P20 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
      H38 GGCGGATGCG CCCACTTTGA GCGTGGATGA CAAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
    Z2491 GGCAGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
      H41 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
    EG329 GGCGGATGCG CCCACTTTGA GCGTGGAT.. .GGGGACGCA TTGAATGTCG GCAGCAAGAA GGACAACAAA
    PMC21 GGCGGATGCG CCCACTTTGA GCGTGGAT.. .GGGGACGCA TTGAATGTCG GCAGCAAGAA GGACAACAAA
    EG327 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
Consensus GGC-GATGCG CCCACTTT-A GCGTGGAT-- ---GG-CGC- TTGAATGTCG GCAGCAAG-A ---CAACAAA
                                               C5

          1471                                                                        1540
      H15 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
     BZ10 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
    BZ198 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
      P20 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
      H38 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
    Z2491 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
      H41 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCG CAACTTAAAG
    EG329 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
    PMC21 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
    EG327 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
Consensus CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGC- CAACTTAAAG
                                               C5

          1541                                                                        1610
      H15 GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
     BZ10 GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
    BZ198 GCGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
      P20 GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGAA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
      H38 GCGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
    Z2491 GCGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
      H41 GTGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGAA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
    EG329 GCGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
    PMC21 GCGTGGCGCA AAACTTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
    EG327 GCGTGGCGCA AAACTTGAAC AACCACATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
Consensus G-GTGGCGCA AAACTTGAAC AACC-CATCG ACAATGTG-A CGGCAACGCG CG-GCGGG-A TCGCCCAAGC
                                               C5

          1611                                                                        1680
      H15 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
     BZ10 GATTGCAACC GCAGGTTTGG CTCAGGCCTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
    BZ198 GATTGCAACC GCAGGTCTAG TTCAGGCGTA TCTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGACACT
      P20 GATTGCAACC GCAGGTTTGG CTCAGGCCTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
      H38 GATTGCAACC GCAGGTCTGG TTCAGGCGTA TCTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGCACT
    Z2491 GATTGCAACC GCAGGTCTGG TTCAGGCGTA TCTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGCACT
      H41 GATTGCAACC GCAGGTCTGG TTCAGGCGTA TCTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGCACT
    EG329 GATTGCAACC GCAGGTCTGG TTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGCACT
    PMC21 GATTGCAACC GCAGGTCTGG TTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGCACT
    EG327 GATTGCAACC GCAGGTCTGG TTCAGGCGTA TCTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGCACT
Consensus GATTGCAACC GCAGGT-T-G -TCAGGC-TA T-TGCCCGGC AAGAGTATGA TGGCGATCGG CGGCG--ACT
                                               C5
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FIG. 2 cont.

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          1681                                                                1750
    H15   TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
   BZ10   TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
  BZ198   TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCAAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
    P20   TATCTCGGCG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
    H38   TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCCAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
  Z2491   TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCCAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
    H41   TATCTCGGCG AAGCCGGTTA TGCCATCGGC TACTCAAGCA TTTCCGCCGG CGGAAATTGG ATTATCAAAG
  EG329   TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCCAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
  PMC21   TATCGCGGCG AAGCCGGTTA CGCCATCGGC TACTCCAGTA TTTCCGACGG CGGAAATTGG ATTATCAAAG
  EG327   TATCGCGGCG AAGCCGGTTA TGCCATCGGC TACTCAAGCA TTTCCGACGG CGGAAATTGG ATTATCAAAG
Consensus TATC-CGGCG AAGCCGGTTA -GCCATCGGC TACTC-AG-A TTTC-G-C-- -GG-AATTGG -TTATCAA-G
                                                                      C5

          1751                                                                1815
    H15   GCACGGCTTC CGGCAATTCG CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
   BZ10   GCACGGCTTC CGGCAATTCG CGCGGTCATT TCGGTACTTC CGCATCTGTC GGTTATCAGT GGTAA
  BZ198   GCACGGCTTC CGGCAATTCG CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAAT GGTAA
    P20   GCACGGCTTC CGGCAATTCG CGCGGTCATT TCGGTACTTC CGCATCTGTC GGTTATCAGT GGTAA
    H38   GCACGGCTTC CGGCAATTCG CGCGGTCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
  Z2491   GCACGGCTTC CGGCAATTCG CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
    H41   GCACGGCTTC CGGCAATTCG CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
  EG329   GCACGGCTTC CGGCAATTCG CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
  PMC21   GCACGGCTTC CGGCAATTCG CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
  EG327   GCACGGCTTC CGGCAATTCG CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTTATCAGT GGTAA
Consensus GCACGGCTTC CGGCAATTCG CGCGG-CATT TCGGT-CTTC CGCATCTGTC GGTTATCA-T GGTAA
                                                                      C5
```

FIG. 2 cont.

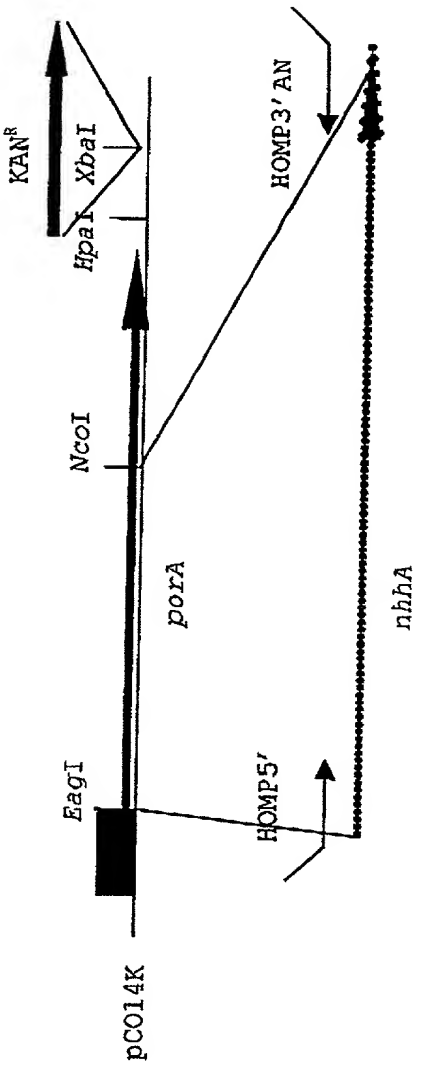

FIG. 3A

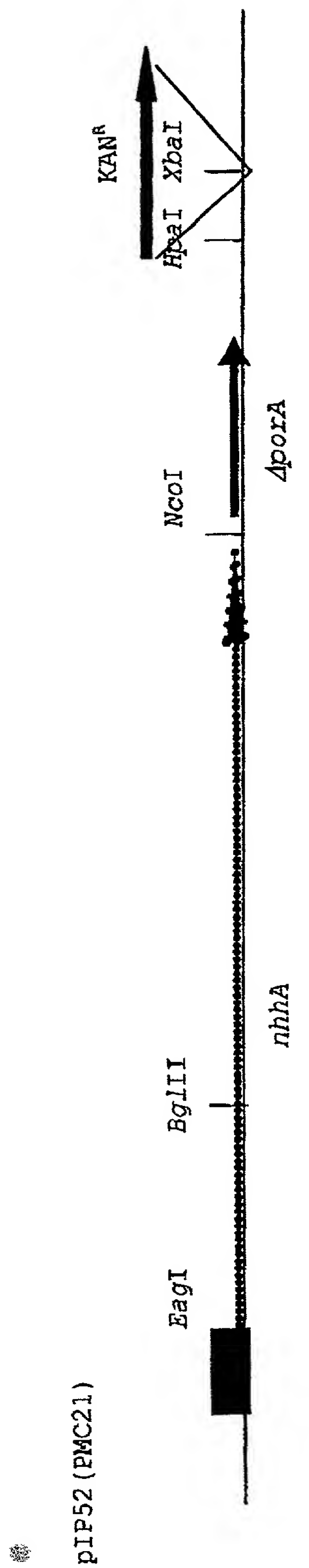

FIG. 3B

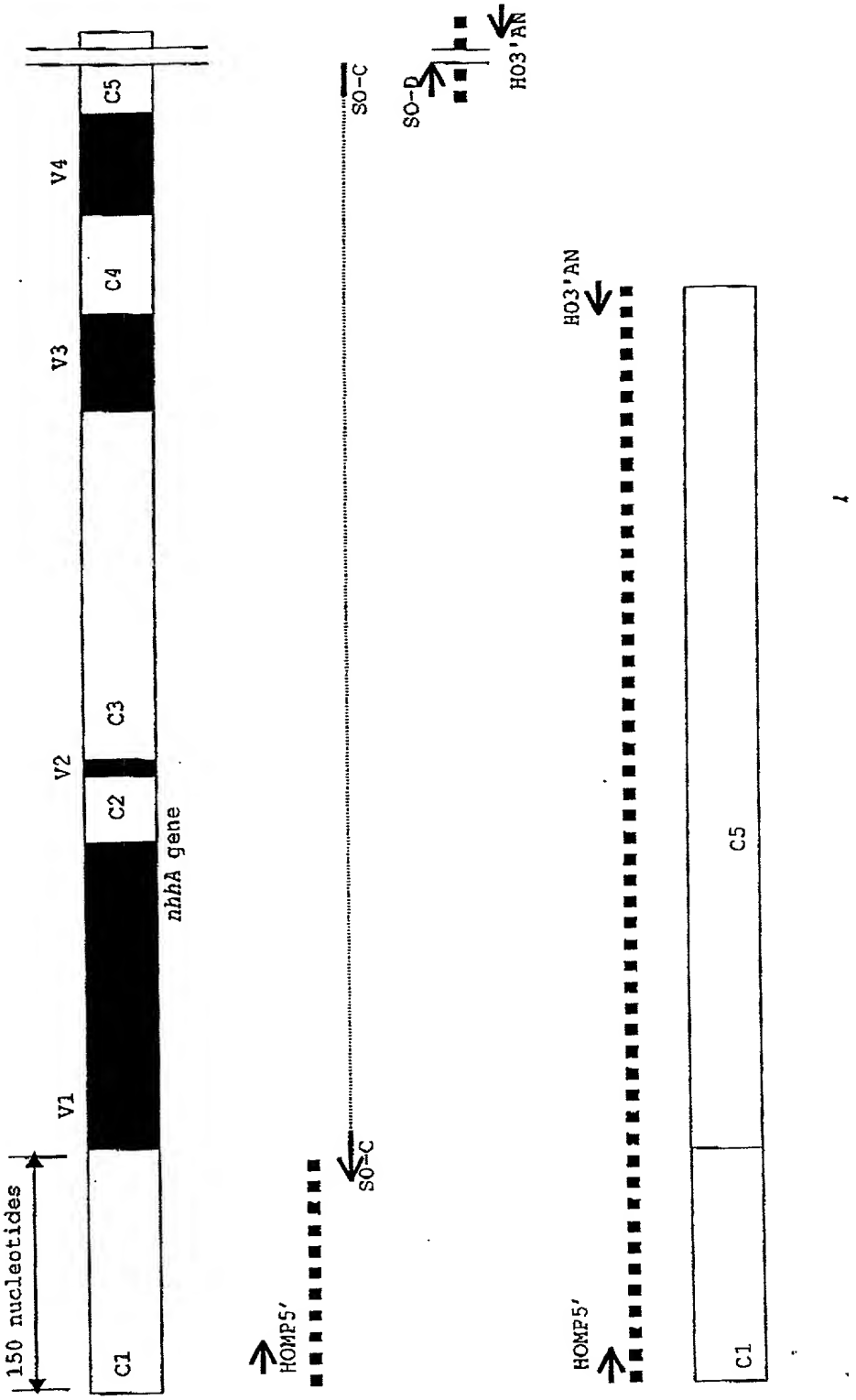
150 nucleotides
C1
V1
C2
V2
C3
nhhA gene
V3
C4
V4
C5
HOMP5'
SO-C
SO-C
SO-D
HO3'AN
HO3'AN
HOMP5'
C1
C5

FIG. 4A

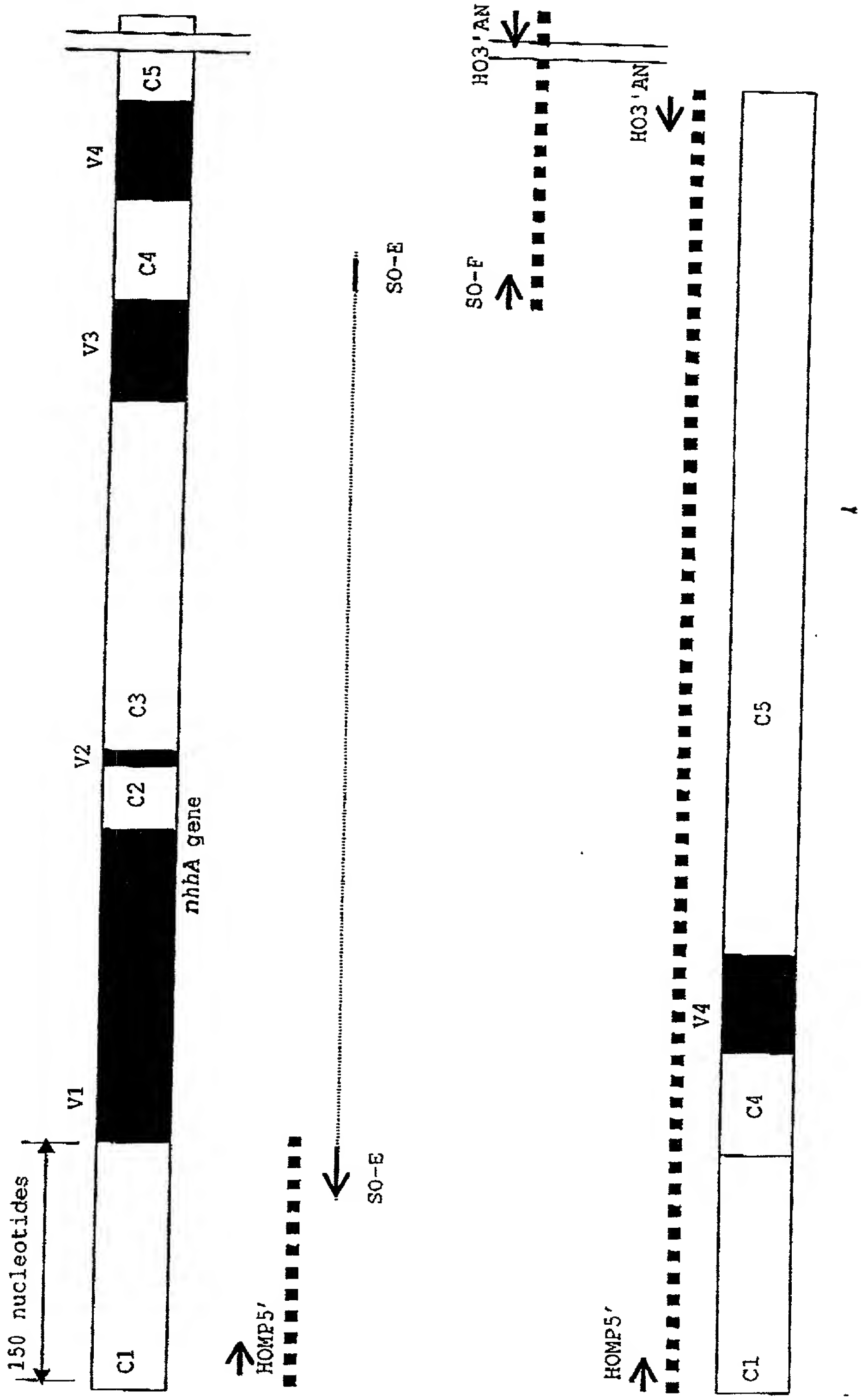
C1
C2
C3
C4
C5
V1
V2
V3
V4
nhhA gene
150 nucleotides
HOMP5'
SO-E
SO-F
HO3'AN

FIG. 4B

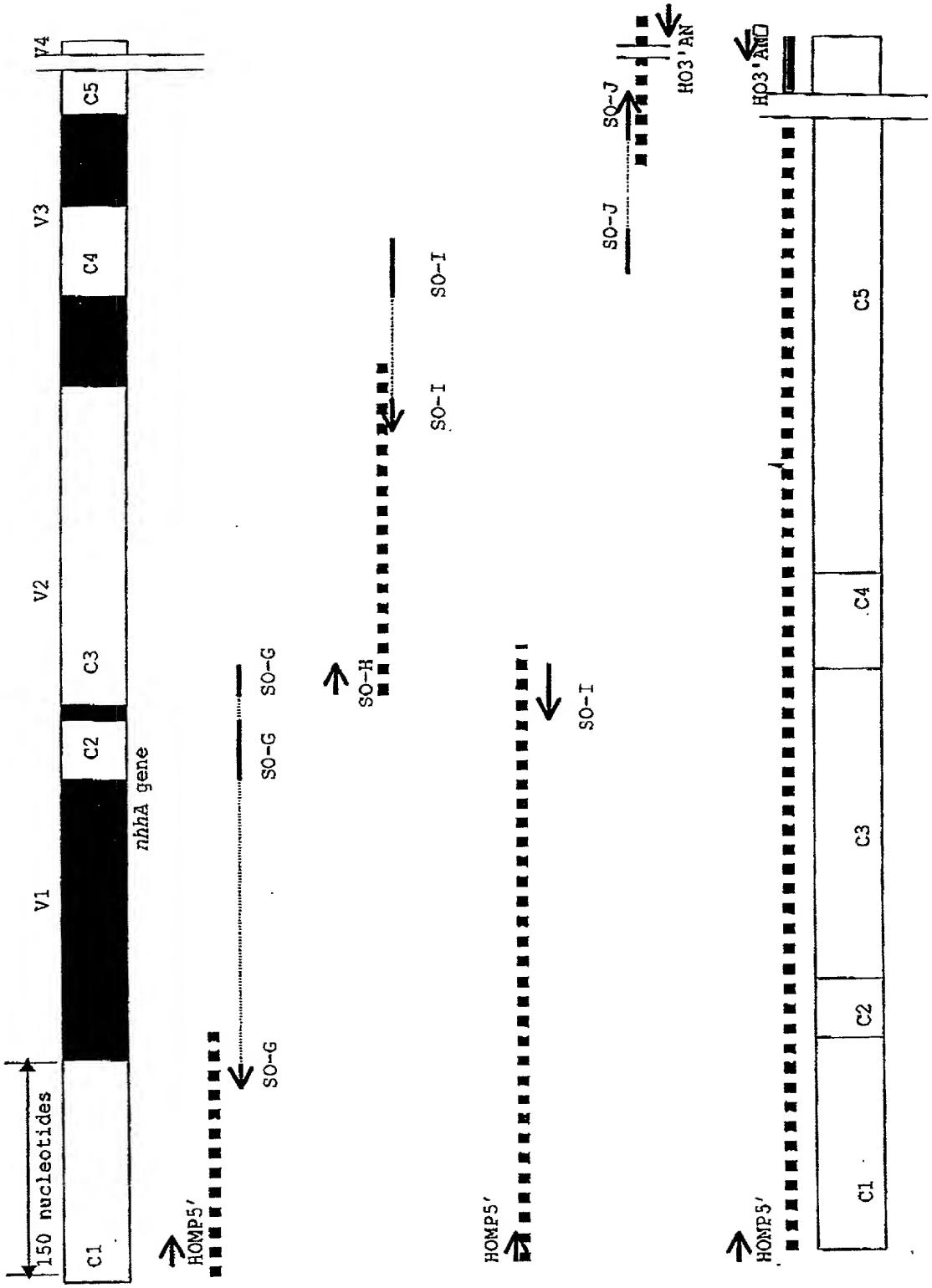
V4
C5
V3
C4
V2
C3
C2
V1
C1
150 nucleotides
nhhA gene
SO-G
SO-G
SO-G
HOMP5'
SO-H
SO-I
SO-I
HOMP5'
SO-I
SO-J
SO-J
HO3'AN
HO3'AND
C5
C4
C3
C2
C1
HOMP5'

FIG. 4C

A

```
  1  MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51  ANNETDLTSV GTEKLSFSAN GNKVNITSDT KGLNFAKETA GTNGDTTVHL
101  NGIGSTLTDT LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKGVK
151  PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201  VIKEKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
251  NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
301  LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE
351  ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
401  RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG
451  LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
501  HFGASASVGY QW*
```

B

```
  1  ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51  CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
101  TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
151  GCTAACAATG AAACAGATCT GACCAGTGTT GGAACTGAAA AATTATCGTT
201  TAGCGCAAAC GGCAATAAAG TCAACATCAC AAGCGACACC AAAGGCTTGA
251  ATTTTGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
301  AACGGTATTG GTTCGACTTT GACCGATACG CTGCTGAATA CCGGAGCGAC
351  CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
401  CAAGCGTTAA AGACGTATTA AACGCTGGCT GGAACATTAA AGGCGTTAAA
451  CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
501  AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
551  GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
601  GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG ACAAAGGCGA
651  GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAAGAAG
701  TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAACCGCT
751  AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
801  AAATGTAACC TTTGCTAGTG GTAAAGGTAC AACTGCGACT GTAAGTAAAG
851  ATGATCAAGG CAACATCACT GTTATGTATG ATGTAAATGT CGGCGATGCC
901  CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAATTTGG ATTCCAAAGC
951  GGTTGCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
1001  AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
1051  ATTACCCGCA ACGGTAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
1101  GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTGAGCG
1151  TGGATGGGGA CGCATTGAAT GTCGGCAGCA AGAAGGACAA CAAACCCGTC
1201  CGCATTACCA ATGTCGCCCC GGGCGTTAAA GAGGGGGATG TTACAAACGT
1251  CGCACAACTT AAAGGCGTGG CGCAAAACTT GAACAACCGC ATCGACAATG
1301  TGGACGGCAA CGCGCGTGCG GGCATCGCCC AAGCGATTGC AACCGCAGGT
1351  CTGGTTCAGG CGTATTTGCC CGGCAAGAGT ATGATGGCGA TCGGCGGCGG
1401  CACTTATCGC GGCGAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCCG
1451  ACGGCGGAAA TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGGC
1501  CATTTCGGTG CTTCCGCATC TGTCGGTTAT CAGTGGTAA
```

FIG. 5

A

```
  1  MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
 51  ATDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
101  NGIGSTLTDM LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKGVK
151  PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201  VIKEKDGKLV TGKGKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
251  NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
301  LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE
351  ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
401  VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
451  GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
501  GHFGASASVG YQW*
```

B

```
   1  ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT
  51  CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101  TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT TCAGGCGAAT
 151  GCTACCGATG AAACAGGCCT GATCAATGTT GAAACTGAAA AATTATCGTT
 201  TGGCGCAAAC GGCAAGAAAG TCAACATCAT AAGCGACACC AAAGGCTTGA
 251  ATTTCGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
 301  AACGGTATCG GTTCGACTTT GACCGATATG CTGCTGAATA CCGGAGCGAC
 351  CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
 401  CAAGCGTTAA AGACGTATTA AACGCAGGCT GGAACATTAA AGGCGTTAAA
 451  CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
 501  AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
 551  GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601  GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG GCAAAGGCGA
 651  GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAAGAAG
 701  TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAACCGCT
 751  AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801  AAAAGTAACC TTTGCTAGTG GTAATGGTAC AACTGCGACT GTAAGTAAAG
 851  ATGATCAAGG CAACATCACT GTTAAGTATG ATGTAAATGT CGGCGATGCC
 901  CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAATTTGG ATTCCAAAGC
 951  GGTTGCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
1001  AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
1051  ATTACCCGCA ACGGCAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
1101  ATTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTAAGCG
1151  TGGATGACGA GGGCGCGTTG AATGTCGGCA GCAAGGATGC CAACAAACCC
1201  GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG ATGTTACAAA
1251  CGTCGCGCAA CTTAAAGGTG TGGCGCAAAA CTTGAACAAC CGCATCGACA
1301  ATGTGAACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT TGCAACCGCA
1351  GGTCTGGTTC AGGCGTATCT GCCCGGCAAG AGTATGATGG CGATCGGCGG
1401  CGGCACTTAT CTCGGCGAAG CCGGTTATGC CATCGGCTAC TCAAGCATTT
1451  CCGCCGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG CAATTCGCGC
1501  GGCCATTTCG GTGCTTCCGC ATCTGTCGGT TATCAGTGGT AA
```

FIG. 6

A

```
  1  MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51  ANNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
101  DGKLVTGKDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
151  QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
201  LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
251  KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV
301  APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
351  LPGKSMMAIG GGTYRGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
401  ASVGYQW*
```

B

```
   1  ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
  51  CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101  TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151  GCTAACAACG TTGATTTCGT CCGCACTTAC GACACAGTCG AGTTCTTGAG
 201  CGCAGATACG AAAACAACGA CTGTTAATGT GGAAAGCAAA GACAACGGCA
 251  AGAAAACCGA AGTTAAAATC GGTGCGAAGA CTTCTGTTAT TAAAGAAAAA
 301  GACGGTAAGT TGGTTACTGG TAAAGACAAA GGCGAGAATG GTTCTTCTAC
 351  AGACGAAGGC GAAGGCTTAG TGACTGCAAA AGAAGTGATT GATGCAGTAA
 401  ACAAGGCTGG TTGGAGAATG AAAACAACAA CCGCTAATGG TCAAACAGGT
 451  CAAGCTGACA AGTTTGAAAC CGTTACATCA GGCACAAATG TAACCTTTGC
 501  TAGTGGTAAA GGTACAACTG CGACTGTAAG TAAAGATGAT CAAGGCAACA
 551  TCACTGTTAT GTATGATGTA AATGTCGGCG ATGCCCTAAA CGTCAATCAG
 601  CTGCAAAACA GCGGTTGGAA TTTGGATTCC AAAGCGGTTG CAGGTTCTTC
 651  GGGCAAAGTC ATCAGCGGCA ATGTTTCGCC GAGCAAGGGA AAGATGGATG
 701  AAACCGTCAA CATTAATGCC GGCAACAACA TCGAGATTAC CCGCAACGGT
 751  AAAAATATCG ACATCGCCAC TTCGATGACC CCGCAGTTTT CCAGCGTTTC
 801  GCTCGGCGCG GGGGCGGATG CGCCCACTTT GAGCGTGGAT GGGGACGCAT
 851  TGAATGTCGG CAGCAAGAAG GACAACAAAC CCGTCCGCAT TACCAATGTC
 901  GCCCCGGGCG TTAAAGAGGG GGATGTTACA AACGTCGCAC AACTTAAAGG
 951  CGTGGCGCAA AACTTGAACA ACCGCATCGA CAATGTGGAC GGCAACGCGC
1001  GTGCGGGCAT CGCCCAAGCG ATTGCAACCG CAGGTCTGGT TCAGGCGTAT
1051  TTGCCCGGCA AGAGTATGAT GGCGATCGGC GGCGGCACTT ATCGCGGCGA
1101  AGCCGGTTAC GCCATCGGCT ACTCCAGTAT TTCCGACGGC GGAAATTGGA
1151  TTATCAAAGG CACGGCTTCC GGCAATTCGC GCGGCCATTT CGGTGCTTCC
1201  GCATCTGTCG GTTATCAGTG GTAA
```

FIG. 7

1	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAS
51	ANRAASVKDV	LNAGWNIKGV	KPGTTASDNV	DFVRTYDTVE	FLSADTKTTT
101	VNVESKDNGK	KTEVKIGAKT	SVIKEKDGKL	VTGKDKGENG	SSTDEGEGLV
151	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK	FETVTSGTNV	TFASGKGTTA
201	TVSKDDQGNI	TVMYDVNVGD	ALNVNQLQNS	GWNLDSKAVA	GSSGKVISGN
251	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID	IATSMTPQFS	SVSLGAGADA
301	PTLSVDGDAL	NVGSKKDNKP	VRITNVAPGV	KEGDVTNVAQ	LKGVAQNLNN
351	RIDNVDGNAR	AGIAQAIATA	GLVQAYLPGK	SMMAIGGGTY	RGEAGYAIGY
401	SSISDGGNWI	IKGTASGNSR	GHFGASASVG	YQW*	

A

1	ATGAACAAAA	TATACCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCATGGGT
51	CGTCGTATCC	GAGCTCACAC	GCAACCACAC	CAAACGCGCC	TCCGCAACCG
101	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT	TCAGGCAAGT
151	GCTAACCGTG	CGGCAAGCGT	TAAAGACGTA	TTAAACGCTG	GCTGGAACAT
201	TAAAGGCGTT	AAACCCGGTA	CAACAGCTTC	CGATAACGTT	GATTTCGTCC
251	GCACTTACGA	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT
301	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG	AAAACCGAAG	TTAAAATCGG
351	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
401	AAGACAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCGA	AGGCTTAGTG
451	ACTGCAAAAG	AAGTGATTGA	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA
501	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG	TTTGAAACCG
551	TTACATCAGG	CACAAATGTA	ACCTTTGCTA	GTGGTAAAGG	TACAACTGCG
601	ACTGTAAGTA	AAGATGATCA	AGGCAACATC	ACTGTTATGT	ATGATGTAAA
651	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT	GCAAAACAGC	GGTTGGAATT
701	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
751	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG
801	CAACAACATC	GAGATTACCC	GCAACGGTAA	AAATATCGAC	ATCGCCACTT
851	CGATGACCCC	GCAGTTTTCC	AGCGTTTCGC	TCGGCGCGGG	GGCGGATGCG
901	CCCACTTTGA	GCGTGGATGG	GGACGCATTG	AATGTCGGCA	GCAAGAAGGA
951	CAACAAACCC	GTCCGCATTA	CCAATGTCGC	CCCGGGCGTT	AAAGAGGGGG
1001	ATGTTACAAA	CGTCGCACAA	CTTAAAGGCG	TGGCGCAAAA	CTTGAACAAC
1051	CGCATCGACA	ATGTGGACGG	CAACGCGCGT	GCGGGCATCG	CCCAAGCGAT
1101	TGCAACCGCA	GGTCTGGTTC	AGGCGTATTT	GCCCGGCAAG	AGTATGATGG
1151	CGATCGGCGG	CGGCACTTAT	CGCGGCGAAG	CCGGTTACGC	CATCGGCTAC
1201	TCCAGTATTT	CCGACGGCGG	AAATTGGATT	ATCAAAGGCA	CGGCTTCCGG
1251	CAATTCGCGC	GGCCATTTCG	GTGCTTCCGC	ATCTGTCGGT	TATCAGTGGT
1301	AA				

B

FIG. 8

A

```
  1  MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51  ANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK
101  GLNFAKETAG TNGDTTVHLN GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD
151  FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIKEKDGKLV
201  TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA NGQTGQADKF
251  ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
301  WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI
351  ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
401  EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS
451  MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY
501  QW*
```

B

```
   1  ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
  51  CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101  TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151  GCTAACACCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AATTCACCTA
 201  CTCGCTGAAA AAAGACCTCA CAGATCTGAC CAGTGTTGGA ACTGAAAAAT
 251  TATCGTTTAG CGCAAACGGC AATAAAGTCA ACATCACAAG CGACACCAAA
 301  GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
 351  TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATCGTGCG GCAAGCGTTA
 401  AAGACGTATT AAACGCTGGC TGGAACATTA AAGGCGTTAA AAACGTTGAT
 451  TTCGTCCGCA CTTACGACAC AGTCGAGTTC TTGAGCGCAG ATACGAAAAC
 501  AACGACTGTT AATGTGGAAA GCAAAGACAA CGGCAAGAAA ACCGAAGTTA
 551  AAATCGGTGC GAAGACTTCT GTTATTAAAG AAAAAGACGG TAAGTTGGTT
 601  ACTGGTAAAG ACAAAGGCGA GAATGGTTCT TCTACAGACG AAGGCGAAGG
 651  CTTAGTGACT GCAAAAGAAG TGATTGATGC AGTAAACAAG GCTGGTTGGA
 701  GAATGAAAAC AACAACCGCT AATGGTCAAA CAGGTCAAGC TGACAAGTTT
 751  GAAACCGTTA CATCAGGCAC AAATGTAACC TTTGCTAGTG GTAAAGGTAC
 801  AACTGCGACT GTAAGTAAAG ATGATCAAGG CAACATCACT GTTATGTATG
 851  ATGTAAATGT CGGCGATGCC CTAAACGTCA ATCAGCTGCA AAACAGCGGT
 901  TGGAATTTGG ATTCCAAAGC GGTTGCAGGT TCTTCGGGCA AAGTCATCAG
 951  CGGCAATGTT TCGCCGAGCA AGGGAAAGAT GGATGAAACC GTCAACATTA
1001  ATGCCGGCAA CAACATCGAG ATTACCCGCA ACGGTAAAAA TATCGACATC
1051  GCCACTTCGA TGACCCCGCA GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC
1101  GGATGCGCCC ACTTTGAGCG TGGATGGGGA CGCATTGAAT GTCGGCAGCA
1151  AGAAGGACAA CAAACCCGTC CGCATTACCA ATGTCGCCCC GGGCGTTAAA
1201  GAGGGGGATG TTACAAACGT CGCACAACTT AAAGGCGTGG CGCAAAACTT
1251  GAACAACCGC ATCGACAATG TGGACGGCAA CGCGCGTGCG GGCATCGCCC
1301  AAGCGATTGC AACCGCAGGT CTGGTTCAGG CGTATTTGCC CGGCAAGAGT
1351  ATGATGGCGA TCGGCGGCGG CACTTATCGC GGCGAAGCCG GTTACGCCAT
1401  CGGCTACTCC AGTATTTCCG ACGGCGGAAA TTGGATTATC AAAGGCACGG
1451  CTTCCGGCAA TTCGCGCGGC CATTTCGGTG CTTCCGCATC TGTCGGTTAT
1501  CAGTGGTAA
```

FIG. 9

```
                1                                                   50
      H41 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
    PMC21 MNKIYRIIWN SALNAWVVVS DLTRNHTKRA SATVNTAVLA TLLFATVQAS
 H41Studel MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
PMC21Bgldel MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 PMC21C1C5 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
                                  C1

               51                                                  100
      H41 ATDED..EEE ELESVQRS.V VGSIQASMEG SVELET...I SLSMTNDSKE
    PMC21 ANNEEQEEYE YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
 H41Studel ATDE..... ..........  .......... .......... ..........
PMC21Bgldel ANNE..... ..........  .......... .......... ..........
 PMC21C1C5 AN ..... ..........  .......... .......... ..........
                                  V1

              101                                                  150
      H41 FVDPYIVVTL KAGDNLKIKQ N.TNENTNAS SFTYSLKKDL TGLINVETEK
    PMC21 GVLTAREITL KAGDNLKIKQ NGTN..... .FTYSLKKDL TDLTSVGTEK
 H41Studel ..........  .......... .......... .......... TGLINVETEK
PMC21Bgldel ..........  .......... .......... .......... TDLTSVGTEK
 PMC21C1C5 ..........  .......... .......... .......... ..........
           V1          C2          V2                  C3

              151                                                  200
      H41 LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
    PMC21 LSFSAHGNKV NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT
 H41Studel LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
PMC21Bgldel LSFSANGNKV NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT
 PMC21C1C5 ..........  .......... .......... .......... ..........
                        C3                                  V3

              201                                                  250
      H41 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
    PMC21 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
 H41Studel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
PMC21Bgldel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
 PMC21C1C5 ..........  .......... .......... .......... ...NVDFVRT
           V3                  C4                  V4      C5

              251                                                  300
      H41 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKG
    PMC21 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD
 H41Studel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKG
PMC21Bgldel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD
 PMC21C1C5 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTGKD
                                  C5

              301                                                  350
      H41 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GQADKFETVT
    PMC21 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GQADKFETVT
 H41Studel KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GQADKFETVT
PMC21Bgldel KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GQADKFETVT
 PMC21C1C5 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GQADKFETVT
                                  C5

              351                                                  400
      H41 SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVGDALNVN QLQNSGWNLD
    PMC21 SGTNVTFASG KGTTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD
 H41Studel SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVGDALNVN QLQNSGWNLD
PMC21Bgldel SGTNVTFASG KGTTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD
 PMC21C1C5 SGTNVTFASG KGTTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD
                                  C5
```

FIG. 10

```
                401                                                 450
H41             SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21           SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
H41Studel       SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21Bgldel     SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21C1C5       SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
                                    C5

                451                                                 500
H41             TPQFSSVSLG AGADAPTLSV DDEGALNVGS KDANKPVRIT NVAPGVKEGD
PMC21           TPQFSSVSLG AGADAPTLSV DG.DALNVGS KKDNKPVRIT NVAPGVKEGD
H41Studel       TPQFSSVSLG AGADAPTLSV DDEGALNVGS KDANKPVRIT NVAPGVKEGD
PMC21Bgldel     TPQFSSVSLG AGADAPTLSV DG.DALNVGS KKDNKPVRIT NVAPGVKEGD
PMC21C1C5       TPQFSSVSLG AGADAPTLSV DG.DALNVGS KKDNKPVRIT NVAPGVKEGD
                                    C5

                501                                                 550
H41             VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA
PMC21           VTNVAQLKGV AQNLNNRIDN VDGNARAGIA QAIATAGLVQ AYLPGKSMMA
H41Studel       VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMA
PMC21Bgldel     VTNVAQLKGV AQNLNNRIDN VDGNARAGIA QAIATAGLVQ AYLPGKSMMA
PMC21C1C5       VTNVAQLKGV AQNLNNRIDN VDGNARAGIA QAIATAGLVQ AYLPGKSMMA
                                    C5

                551                                                 600
H41             IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21           IGGGTYRGEA GYAIGYSSIS DGGNWIIKGT ASGNSRGHFG ASASVGYQW.
H41Studel       IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21Bgldel     IGGGTYRGEA GYAIGYSSIS DGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21C1C5       IGGGTYRGEA GYAIGYSSIS DGGNWIIKGT ASGNSRGHFG ASASVGYQW.
                                    C5
```

FIG. 10 cont'd

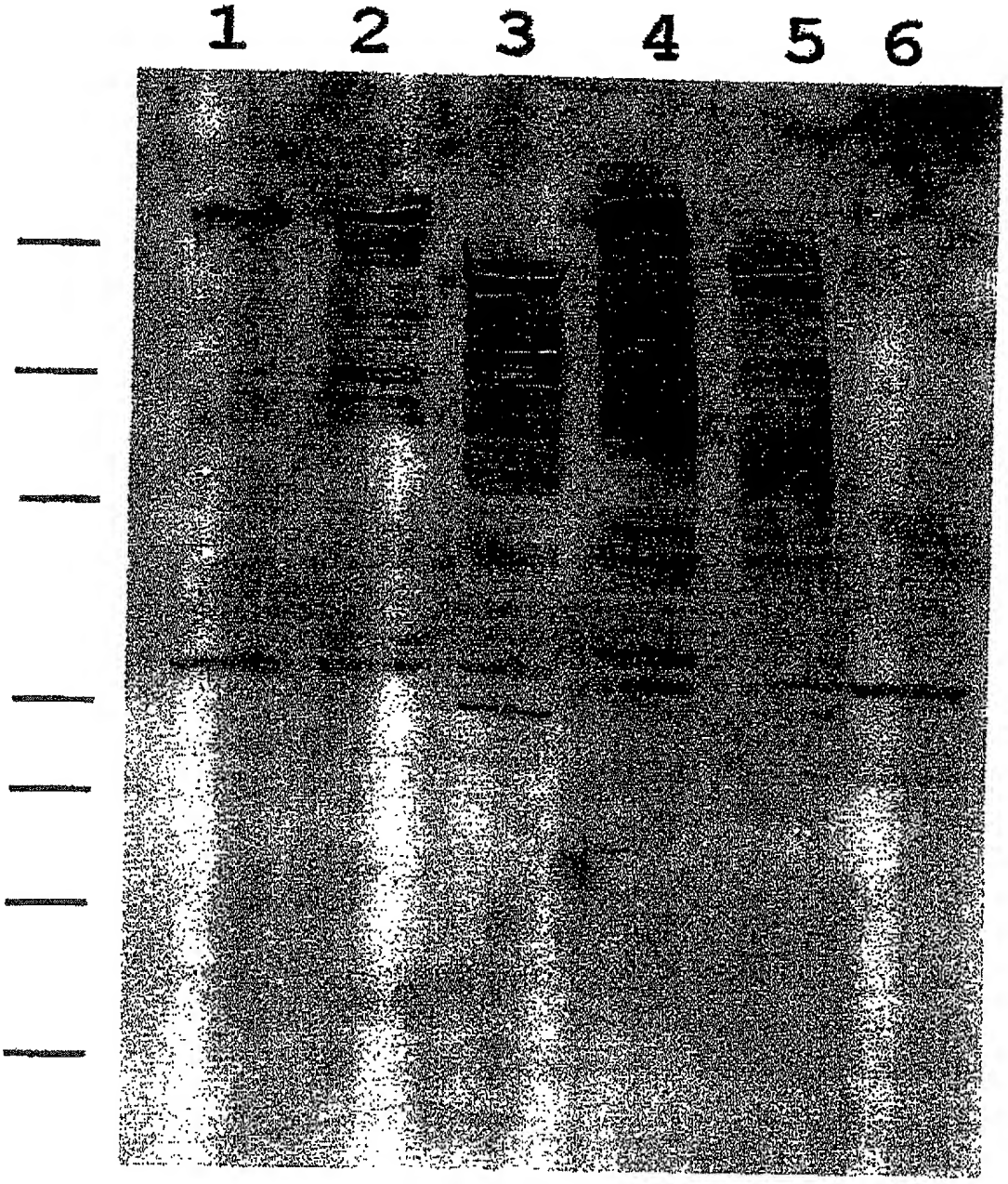

FIG. 11

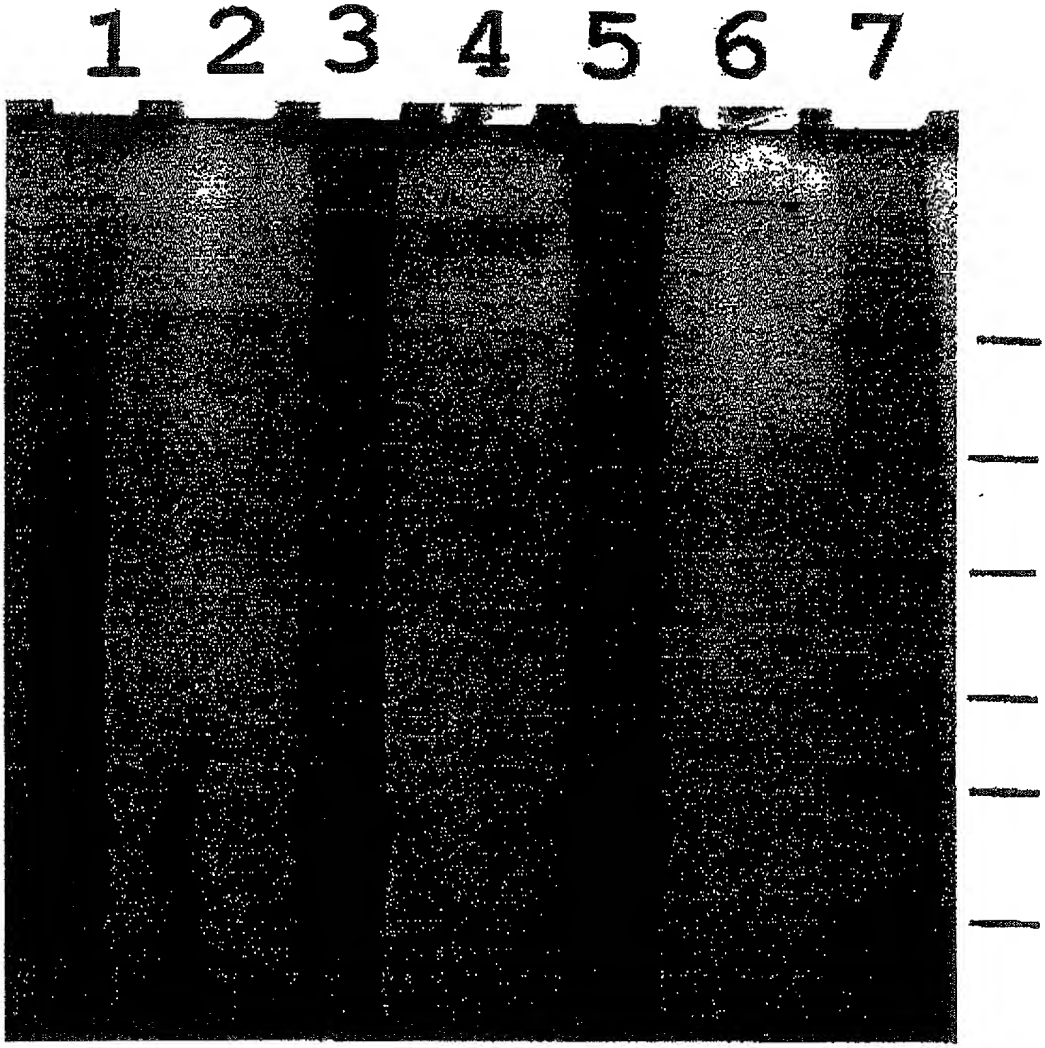

FIG. 12

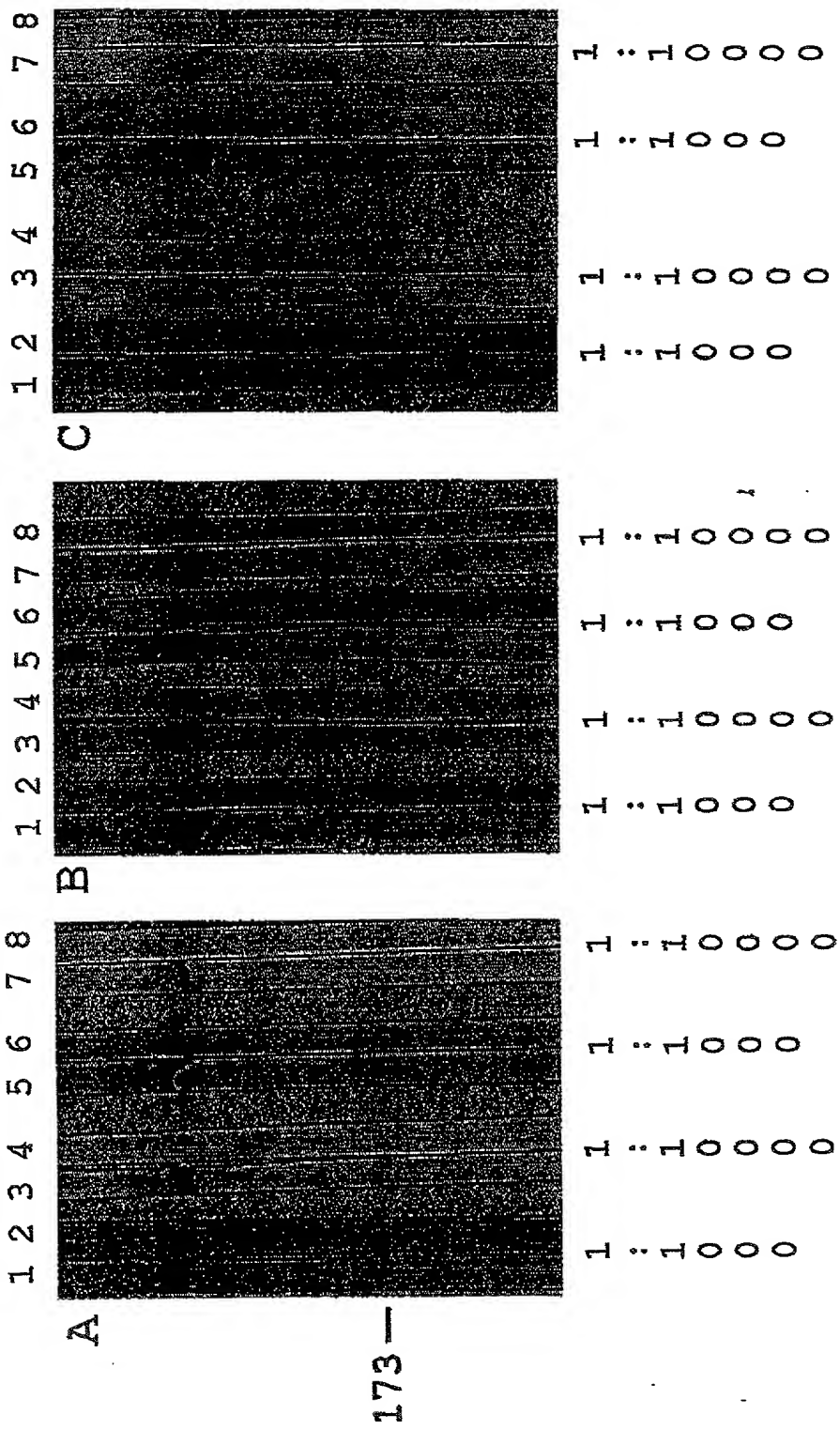
1 2 3 4 5 6 7 8
1 : 10000
1 : 1000
1 : 10000
1 : 1000
C
1 2 3 4 5 6 7 8
1 : 10000
1 : 1000
1 : 10000
1 : 1000
B
1 2 3 4 5 6 7 8
1 : 10000
1 : 1000
1 : 10000
1 : 1000
A
173

FIG. 13

A

```
 52   NNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
101   GVLTAREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSAHG
151   NKVNITSDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL LNTGATTNVT
201   NDNVTDDEKK RAASVKDVLN AGWNIKGVKP GTTASDNVDF VRTYDTVEFL
251   SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGKLVT GKDKGENGSS
301   TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF
351   ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
401   SGKVISGNVS PSKGKMDETV NINAGNNIEI TRNGKNIDIA TSMTPQFSSV
451   SLGAGADAPT LSVDGDALNV GSKKDNKPVR ITNVAPGVKE GDVTNVAQLK
501   GVAQNLNNRI DNVDGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG
551   EAGYAIGYSS ISDGGNWIIK GTASGNSRGH FGASASVGYQ W*
```

B

```
 52   TDEDEEEEL ESVQRSVVGS IQASMEGSVE LETISLSMTN DSKEFVDPYI
101   VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTGLINVE TEKLSFGANG
151   KKVNIISDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDML LNTGATTNVT
201   NDNVTDDEKK RAASVKDVLN AGWNIKGVKP GTTASDNVDF VRTYDTVEFL
251   SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGKLVT GKGKGENGSS
301   TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTKVTF
351   ASGNGTTATV SKDDQGNITV KYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
401   SGKVISGNVS PSKGKMDETV NINAGNNIEI TRNGKNIDIA TSMTPQFSSV
451   SLGAGADAPT LSVDDEGALN VGSKDANKPV RITNVAPGVK EGDVTNVAQL
501   KGVAQNLNNR IDNVNGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYL
551   GEAGYAIGYS SISAGGNWII KGTASGNSRG HFGASASVGY QW*
```

FIG. 14

C

```
 52   NNETDLTSV GTEKLSFSAN GNKVNITSDT KGLNFAKETA GTNGDTTVHL
101   NGIGSTLTDT LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKGVK
151   PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201   VIKEKDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
251   NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
301   LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE
351   ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
401   RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG
451   LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
501   HFGASASVGY QW*
```

D

```
 52   TDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
101   NGIGSTLTDM LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKGVK
151   PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201   VIKEKDGKLV TGKGKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
251   NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
301   LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE
351   ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
401   VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
451   GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
501   GHFGASASVG YQW*
```

FIG. 14

E

```
 52   NNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
101   DGKLVTGKDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
151   QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
201   LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
251   KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV
301   APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
351   LPGKSMMAIG GGTYRGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
401   ASVGYQW*
```

F

```
 52   NRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
101   VNVESKDNGK KTEVKIGAKT SVIKEKDGKL VTGKDKGENG SSTDEGEGLV
151   TAKEVIDAVN KAGWRMKTTT ANGQTGQADK FETVTSGTNV TFASGKGTTA
201   TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS GWNLDSKAVA GSSGKVISGN
251   VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA
301   PTLSVDGDAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN
351   RIDNVDGNAR AGIAQAIATA GLVQAYLPGK SMMAIGGGTY RGEAGYAIGY
401   SSISDGGNWI IKGTASGNSR GHFGASASVG YQW*
```

G

```
 50 SANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK
101   GLNFAKETAG TNGDTTVHLN GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD
151   FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIKEKDGKLV
201   TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA NGQTGQADKF

251   ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
301   WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI
351   ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
401   EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS
451   MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY
501   QW*
```

FIG. 14